Page 1

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GenCore version 5.1.6
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	August 14, 2003, 11:14:25; Search time 6119 Seconds (without alignments) 10783.989 Million cell updates/sec
Title: Perfect score: Seguence:	US-09-647-841B-1 1613 1 ttttataaatatttaagctttgaacttgagtaccttactc 1613
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 seqs, 20454813386 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

5777422

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 GenEmbl:*

11 gb_ba;*
21 gb_htg:*
31 gb_htg:*
41 gb_om:*
51 gb_ov:*
61 gb_ph;*
61 gb_ph;*
62 gb_ph;*
63 gb_ph;*
64 gb_ph;*
65 gb_ph;*
65 gb_ph;*
66 gb_ph;*
67 gb_ph;*
68 gb_ph;*
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Pred. No. 1s the number of results predicted by chance to have a

em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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TPCPPPLVPYPPTPAQQTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGL
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Bastola, D.R., Pethe, V.V. and Winicov, I.

Alfini, a novel zinc-finger protein in alfalfa roots that binds promoter elements in the salt-inducible MsPRP2 gene Plant Mol. Biol. 38 (6), 1123-1135 (1998)
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Post-transcriptional regulation of a salt-inducible alfalfa encoding a putative chimeric proline-rich cell wall protein plant Mol. Biol. 27 (2), 411-418 (1995) 7888629
                                                                                                                                                                                           Direct Submission
Submitted (06-OCT-1997) Microbiology and Biochemistry, Univol Nevada, Reno, 320, Reno, NV 89557, USA
On Nov 1, 1998 this sequence version replaced gi:559012.
Location/Qualifiers
i. 3617
/ Organism="Medicago sativa"
/ Mol_type="genomic DNA"
/ Cultivar="Apollo"
/ Ab_xref="taxon:3879"
/ Clone_NsPRP2"
/ Clone_NsPR2"
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; Mismatches. 20;
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Best Local Similarity 94.9%;
Matches 1510; Conservative
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BX088600 195620 bp DNA linear HTG 02-JUN-2003 Danio rerio clone DKEY-166M7, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.
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 340 TTAAGCATATAAACATCAAAGTCTAAAACTAGCAAAATGTTGTTTTAGGATGACAATT 399
                                                                                                                                                                                                                                                                                                                                                              Submitted (29-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgesiare, CB10 1SA, UK. E-mail enquiries: CB163-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on MAY 11, 2003 this sequence version replaced g1:29500441.
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1 (Spariniformes; Lto 195620)
Mclaren,S.
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                                                                                                                                                                                                            512 GATTAAGATTGCCCCTTTCATCACGGGTCGAATAATAGCACTACTTGTCACTACATGT
                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Danio rerio (zebrafish)
Danio rerio
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (02-JUN-1992) D.P. Bown, University of Durham, Dept. of
Biological Sciences, Science Site, South Rd, Durham, DHI 3LE, UK
Location/Qualifiers
                                                       TCATAGTACACTACATTTCTTTGAAACATGGCTAACTATGCTCTAGCCAATGTTTT
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                                                                                                                             1583 CATCCTTCTTTGAACTTGAGTACCTTACTC 1613
                                                                                                                                                 1582 CATCCTTCTTGAACTTGAGTACCTTACTC 1612
                                                                                                                                                                                                                                                                    DNA
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858. .863
944. .2002
/gene="ptxA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA47812.1"
/db_xref="GI:2578444"
                                                                                                                                                                                                                                                                  3234 bp
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944. .1015
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/gene="ptxA"
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665 c
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Pisum sativum (pea)
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Homo sapiens chromosome 1 clone RP5-916c24, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Mar 11, 2001 this sequence version replaced gi:9931646.
                                                      AATA-AGGTTCATTGGTTAAAAAACTAAAAATAATTTCTCTCCTGATTTATATGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 128569; sum-of-contigs
Insert size: 130251; 3.5% error; agarose-fp
Quality coverage: 8.06x in Q20 bases; sum-of-contigs Quality
coverage: 8.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 128305 bases at least Q30
Consensus quality: 128455 bases at least Q30
Consensus quality: 128526 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 40557: contig of 7165 bp in length
58 40757: gap of 100 bp
58 128769: contig of 88012 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33392: contig of 33392 bp in length 33492: gap of 100 bp
                                                                                                                                                   GACATTTTTTGGAACATGAAGGGTATTGATTTTT 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-5"
1. 33392
/note="assembly_fragment:01246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: dJ916C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- Summary Statistics
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HTG: HTGS_PHASE1; HTGS_CANCELLED.
HOMO sapiens (human)
HOMO sapiens
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP5-916C24"
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40658
40758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 TATAATTTACATGCCGTTACGGTAAAAATGGATAAATTGGGTATGGAGTACTAGTAATT 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGYGCCATTCACGATTCTTCTTGGTGCAGCTTGGAGAACCCTATCCTGGGCTTGGAAGA
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               gap of 100 bp
contig of 48497 bp in length
gap of 100 bp
contig of 35683 bp in length
                                                                                     100 bp
of 34959 bp in length
68521 bp in length
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                                                                                                                                             contig of 7560 bp in length
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Pred. No. 3.9e-07;
                                                                                                                                                                                    1. .195620
//organism="Danio rerio"
//organism="Danio rerio"
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/clone="DkRY-166M7"
/clone="DkRY-166M7"
/clone="Lb="DanioKey"
1. .68521
//note="assembly_fragment:00804
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68622 .117118
//note="assembly_fragment:01509
fragment_chain:1"
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/note-"assembly_fragment:00046
fragment_chain:1"
153002: .187960
/note-"assembly_fragment:01399
fragment_chain:1"
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/note="assembly_fragment:00747
/ragment_chain:1
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35078 c 35193 g 64578 t
                                                                                                                            100 bp
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gap of 100
                                                                                                                                                                 ocation/Qualiflers
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153001:
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Similarity 50.6%;
21; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                               187 TGATGGTAAAAAAAAAAATATATATTTGTTACCATTTAAAAGTCATAAAATATAGTACAATC 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         607 GTTAAAAAAACTAAAAAATAATTTCTCTCTGATTTATATGAAATGACATTTTTTGGAA 666
                                                                                                                                                                                                  7 AAATATTTAAGCTTGATAATATTTTGCGATCTATATATAAGCCCACTACCAATTTAAAA 66
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Homo sapiens chromosome 8, clone CTD-3118D11, complete sequence.
ACO84128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAAAAAAAAAGTCATAAATATAGTTTATACATATAACTTTAATAAAAAATA
                                                                                                                                                         DB 2; Length 128769;
                                                                                                                       200 others
                                                                                                                                                                             Indels
                                                                                                                                                      7.2%; Score 115.6; DB 2;
43.8%; Pred. No. 8.5e-07;
Live 0; Mismatches 374;
                           % 3493. ...40657

/note="assembly_fragment:00130

fragment_chain:1"

40758. .128769

/note="assembly_fragment:01367

fragment_chain:1

clone_end:sp6

vector_side:right"

a 24900 c 24955 g 38655 t 2
                    vector_side:left"
fragment_chain:1
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           clone_end:T7
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Bulkaryora Neatons (human)

Bulkaryora Neatons (human)

Bulkaryora Neatons (hondata Canalata, Vertebrata; Enteleostoni, Bulkaryora Neatons, Charles (1) Triances; Catarrillai, Hominidae Homo.

Bulkaryora Neatons (1) Triances; Catarrillai, Forminidae Homo.

Bulkaryora Neatons (1) Triances; Catarrillai, Forminidae Homo.

Bulkaryora Neatons (1) Triances; Catarrillai, Forminidae Homo.

Bulkaryola Neatons (1) Triances; Catarrillai, Forminidae (1) Triances; Catarrillain (1) Triances; Catarrillain (1) Triances; Catarrillain (1) Triances; Catarrillain (1) Triances; R. Linders (1) Triances; R. Triance
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Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Starge-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (30-301-2002) Whitehead Institute/MIT Center for Genome Submitted (30-302-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 30, 2002 this sequence version replaced g1:21306731.

All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions&genome.wi.mit.edu
Contact: project Information
Center project name: 1.11383
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32790 9 TCCAACCCTTTGAGAGGTTAATGTGTGTGCGGATTTTCTAGATAAACAAGGYGCCATTCA 304 185 GTTGATGGTAAAAAAATAAATTATAATTTGTTACCATTTAAAAGTCATAAATATATAGTACAA 17; Gaps Length 129240; Indels Query Match 7.1%; Score 114.6; DB 9; Best Local Similarity 48.7%; Pred. No. 1.1e-06; Matches 491; Conservative 1; Mismatches 500; /rpt_family="MER41A" /rpt_family="MER41A" /rpt_family="Alu3b" /rpt_family="Alu3b" complement(22240...22864)
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                                                                                                                      TCCTACCANAAAAAAAAAGTCATAAATATAGTTTATACATATAACTTTAATAAAAATAA
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Patent: WO 02077272-A 386 03-OCT-2002;
Epigenomics AG (DE)
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Sequence 386 from Patent WO02077272.
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AUTHORS
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AC104790 123589 bp DNA linear PRI 29-MAY-2002
Homo sapiens BAC clone RP11-167A8 from 4, complete sequence.
AC104790
CAATATTATAAAGCTTCATAGCATGTGGATATTCATTTAGAAATATAGATTAGATTGCCC 1020
                                                                                                                                                                                                                                                                                                                                                                                  1260 GGGCCCACATATAAATCCATGAAGGATTTCAAT-GTCCATCCAAGTCAATGATTCAACAT 1318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                       543
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Catarrhini; Hominidae; Homo.
                                                                        CTTTCATCACGGGTCTAACAGCACCACTTGTCACTACATGTCAAAAATGTCCTCTAGTAC
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                                  Direct Submission
Submitted (21-DEC-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
4 (bases 1 to 123589)
Waterston, R. H.
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Center code: WUGSC
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The sequence of Homo sapiens BAC clone RP11-167A8
Unpublished (2001)
3 (bases 1 to 123589)
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Genome Res. 8 (11), 1097-1108 (1998)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
I (bases 1 to 123589)
Sulston, J. E. and Waterston, R.
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Homo sapiens
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Web site: http://genome.wustl.edu/gsc

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The clone sequenced to the left is RP11-460L16; the clone sequenced to the right is RP11-162Fi, 2000 bp overlap. Actual start of this clone is at base position 41945 of RP11-460L16; actual end is at base position 44749 of RP11-162Fi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Louis
                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An Improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. IMO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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Location/Qualifiers
1. 12589
/organism="Homo sapiens"
/mol_type="genomic DNA"
/chromosome="4"
Contact: saplens@watson.wustl.edu
                                                  Center project name: H_NH0167A08
                          Summary Statistics
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/clone_11b="RPCI-11"
353 379
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27744. .28416
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18233. 18267
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5483. .15742
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                                                                                                                                                                                                                                                                                      173 TATATTTA, TTACGTTGATGGTAAAAAATAAATATAATTTGTTACCATTTAAAAGTCATA
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                                                                                                                                                                                                                     Length 123589;
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                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                     Query Match 7.0%; Score 113.2; DB 9; Best Local Similarity 49.5%; Pred. No. 1.8e-06; Matches 380; Conservative 0; Mismatches 378;
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SOURCE

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173 TATATTATTACGTTGATGCTAAAAAATAAATAATTTGTTACCATTTAAAAGTCATA 232
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                                                                                                                                                                                       172758: contig of 131656 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.6e-06;
0; Mismatches 378; Indels
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                                              12324: contig of 6293 bp in length
12424: gap of 100 bp
20299: contig of 7875 bp in length
20399: gap of 100 bp
41002: contig of 20603 bp in length
41102: gap of 100 bp
                       100 bp
of 6293 bp in length
    contig of 1775 bp in length
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1. .1040
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30643 c 31348 g 54356 t
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4157. .5931
/note-"assembly_fragment"
6032. .12324
/note-"assembly_fragment"
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                                                                                                                                                                                                            Location/Qualifiers
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                              gap of
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                                                                                                                                                                                                                                                                                                                                                    /map-"4"
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       4157
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6032
12325
12425
20400
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41103
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                                                                                                                                                                                                                                                                                                     Uppublished

S (bases 1 to 172758)

S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Badakhi, J., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Coepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Foriest, C., Castle, A., Ferreira, P., Fitzhugh, M., Foriest, C., Collymore, A., Cooke, P., Farreira, P., Fitzhugh, W., Foriest, C., Cally, Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., McGurk, A., Marquis, N., Marquis, N., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., Mencus, L., Morrow, J., Nallor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Plerre, N., Pisani, C., Pollara, V., Raymond, C., Rliey, R., Rothman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Wassillev, H., Yiel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Lienct, Submission Nhitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7657780.

All repeats were identified using RepeatMasker:
Smit, A. F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/Rw/RepeatWasker:html
AC022553 172758 bp DNA linear HTG 26-MAY-2000 Homo sapiens chromosome 4 clone RP11-167A8 map 4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: 167_A_8

Center clone name: 167_A_8

Genter clone name: 167_A_8

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 166954 bases at least 040

Consensus quality: 171275 bases at least 030

Consensus quality: 171275 bases at least 020

Insert size: 182000; agarose-fp

Insert size: 182000; syarose-fp

Insert size: 172058; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 5.5 in Q20 bases; agarose-fp
Quality coverage: 5.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of 1040 bp in length
gap of 100 bp
contig of 1580 bp in length
gap of 100 bp
contig of 1236 bp in length
gap of 100 bp
                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-167A8 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                 AC022553 GI:8072485
AC022553.3 GI:8072485
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens (human)
                                                                                                                                                                                                                          (bases 1 to 172758)
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1141
2721
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4057
LOCUS
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AUTHORS
TITLE
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AUTHORS
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JOURNAL
                                                                    ACCESSION
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KEYWORDS
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COMMENT

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293 AGGYGCCA!TCACGATTCTTGTTGGTGCAGCTTGGAGAACCCTATCCTGGGCTTGGAAGA 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AATATAGTNCAATCCAACCCTTTGAGAGGTTAATGTGTGTGCGGATTTTCTAGATAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 159948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
               2991 32990; gap of 100 bp

1991 49822: contig of 16832 bp in length

1992 55063: contig of 5141 bp in length

1994 55163: gap of 100 bp

1994 55163: gap of 100 bp

1994 111844: contig of 56681 bp in length

1995 131419: contig of 19475 bp in length

1420 131519: gap of 100 bp

1420 131519: gap of 100 bp

1430 1349 of 100 bp

1431 159948: contig of 17511 bp in length

1131 159948: contig of 10818 bp in length.

100 1131 159948: contig of 10818 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     701 others
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   bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 112.8; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_side.left"
3209. 32890
Anote="assembly_fragment:01691
fragment_chain:1"
3291. 49822
Anote="assembly_fragment:00994
fragment_chain:1"
4923. 55063
Anote="assembly_fragment:00405
fragment_chain:1"
5364. 111844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:00672"
149131. 159948
/note="assembly_fragment:00468
                                                                                                                                                                                                                                                                                                                                                                                 1. .3108
//oote= assembly_fragment:01033
fragment_chain:1
clone_end:SP6
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/hote="assembly_fragment:00155
fragment_chain:1"
131520. .149030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment:01949"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector_side:right"
27454 c 27877 g 52417 t
                                                                                                                                                                                                                                                                                     /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-162119"
                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CHORI-211"
   contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:T7
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319; Conservative
                                     32991
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Matches 31
                                                                                                                                                                                                                                                                       source
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                                   84197
                                                                                                                                                                                                                                                                                                                                         BX248240 159948 bp DNA linear HTG 03-APR-2003
Danio rerio clone CH211-162119, *** SEQUENCING IN PROGRESS ***, 8
                                                                                                                                                                                                                               712
                                                                                                                                                                                                                                                                                                       772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Scrinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                         84252 TATATATATATTATATATATTATATATATATTT----ATATATATTTTATATATTT
TATAATTTACATGCCGTTACGGTAAAAAATGGGTAAATTGGGGTATGGAGTACTAGTAATT
                                                                                                                                                   AATAAGGTTCATTGGTTAAAAAAACTAAAAAATAATTTCTCTCCTGATTTATATGAAATG
                                                                                                                                                                                                                           653 ACATITITIGGAACAIGAAGGGTATITGATTTTACCACCTTTTACACCTTTCAAAGCCA
                                                                                                                                                                                                                                                                                                       713 TTCAAGGATGAATATAGATTTTTGGGCGATCAAACACAGAATCATTACGATAACATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGR4; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 156495 bases at least 040 Consensus quality: 157186 bases at least 040 Consensus quality: 157186 bases at least 020 Insert size: 159248; sum-of-contigs of Insert size: 15025; 6.7% error; agarose-fp Quality coverage: 9.26x in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                    TATACATACCCCGTCAATCTTCTTTTTTTACCCAATAAACATTGAAA 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3108: contig of 3108 bp in length 3208: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX248240.3 GI:29539163
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Danlo rerio (zebrafish)
Danlo rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coverage: 9.80x in Q20 bases; agarose-fp
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473
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BX248240/c
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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Gaps

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233 AATATAGTACAATCCAACCCTTTGAGAGGTTAATGTGTGCGGATTTTCTAGATAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGYGCCATTCACGATTCTTGGTGCAGCTTGGAGAACCCTATCCTGGGCTTGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCATCCTTCCTACCAAAAAAAAAAAAGTCATAAATATAGTTTATACATAAACTTTAAAT
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 not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 187310;
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                                                                                                         98162: contig of 98162 bp in length
98262: gap of 100 bp
132235: contig of 36973 bp in length
135335: gap of 100 bp
140884: contig of 5549 bp in length
140984: gap of 100 bp
187310: contig of 46326 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 112.8; DB 2; Length
Pred. No. 1.8e-06;
0; Mismatches 282; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          vector_side:left"
98263. 135235
7note="assembly_fragment:03318
fragment_chain:1"
135336. 140884
/note="assembly_fragment:02018
fragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:01818
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment:02183
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a 32428 c 32250 g 60743 t
                                                                                                                                                                                                                                                                            /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-134Dil"
                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CHORI-211"
                                                                                                                                                                                                                                         Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector_side:right"
140985. .187310 ...
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Matches 290; Conservative
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98263
135236
135336
140885
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*** SEQUENCING IN PROGRESS ***, 4
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                                                                                                                                                                                                                                                                                                                                                                        711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (29-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
Submittedshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 2, 2003 this sequence version replaced gi:28272911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Actinopterygil; Neopterygil; Teleostel; Ostariophys1; Cyprinformes; Cyprinfidae; Danio.

1 (bases 1 to 187310)
Mclaren,S.
                                  TTATAATTTACATGCCGTTACGGTAAAAATGGATAAATTGGGTATGGAGTACTAGTAAT
                                                                                                                                                                                                                                               TAATAAGGTTCATTGGTTAAAAAACTAAAAAATAATTTCTCTCCTGATTTATATGAAAT
TTTACTTCTTGTTGATGCTTCTAGAGTACAGCTCCTTAAGGCTGTAGTCTAGTTTTTTT
                                                                      TTCATCCTTCCTACCAAAAAAAAAAAAGTCATAAATATAGTTTATACATATAACTTTAAT
                                                                                                                                             473 AAAAATAAAAAATTTCATCCCTAAAAACATAGTAGAAAT-TTCATAAAAAAATATTGT
                                                                                                                                                                                                                                                                                                                                                                    652 GACATTTTTTGGAACATGAAGGGTATTTGATTTTTACCACCTTTTACACCTTTCAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                           712 ATTCAAGGATGAATATAGATTTTTGGGCGATCAACACAAGAATCATTACGATAACATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 187010; sum-of-contigs
Insert size: 190203; 4.5% error; agarose-fp
Quality coverage: 9.35x in Q20 bases; sum-of-contigs Quality
coverage: 9.31x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently * consists of 4 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 184982 bases at least Q40
Consensus quality: 185170 bases at least Q40
Consensus quality: 185407 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BX005122
BX005122.7 GI:29500520
HTG: HTGS_PHASE1; HTGS_RAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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TITLE
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BX005122
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55743 ATAAAATAATATATAAATAATAATAAAAAATAATATATAATAATAATTAATAATTAATAATTAATAAA 55684
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                                                                                                                                                                                                                                                                                                       533 TATAATTTACATGCCGTTACGGTAAAAATGGATAAATTGGGTATGGGTACTAGTAATT
                                                                                                                                                                                                                                                                                173 TATATTTAKTACGTTGATGGTAAAAAAATAAATATAATTTGTTACCATTTAAAAGTCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 AATATAGTNCAATCCAACCCTTTGAGAGGTTAATGTGTGTGCGGATTTTCTAGATAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 AGGYGCCATTCACGATTCTTGTTGTGCAGCTTGGAGAACCCTATCCTGGGCTTGGAAGA
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Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B.,
Cook, D., Kim, D. and Roeb, B.A.
Medicago truncatula BAC Clone mth2-30j23
                                                                                                                                                                                                Length 178066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC123976 Inncatula clone mth2-30j23, complete sequence. AC123976
                                                                           /note="assembly_fragment:01949"
162125. 178066
/note="assembly_fragment:02276.0"
a 30938 c 31644 g 58405 t 300 others
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                                                                                                                                                                                              Score 112.2; DB 2;
Pred. No. 2.1e-06;
0; Mismatches 283;
              /note="assembly_fragment:00210
fragment_chain:1"
76635. 162024
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55475. .76534
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al Similarity 50.8%;
293; Conservative
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                                            bxu04966 178066 bp DNA linear HTG 03-MAR-2003 Danio rerio clone DKEY-5E12, *** SEQUENCING IN PROGRESS ***, 4 UNDOCCECES 1.000
                  533 TATAATTTACATGCCGTTACGGTAAAAATGGATAAATTGGGTATGGAGTACTAGTAATT 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: Estish-helpgeanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Mar 3, 2003 this sequence version replaced g1:27502002.
                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 178066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 176844 bases at least Q40 Consensus quality: 177008 bases at least Q30 Consensus quality: 17701 bases at least Q20 Insert size: 177766; sum-of-contigs Insert size: 164152; 6.3% error; agarose-fp Quality coverage: 11.15x in Q20 bases; sum-of-contigs Quality coverage: 11.15x in Q20 bases; sum-of-contigs Quality
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BX004966.5 GI:28803915
HTG: HTGS_PHASE1: HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                    98107 AATAAAAAAATTAATAAAAATATAATTAAT 98139
                                                                                              593 AATAAGGTTCATTGGTTAAAAAAACTAAAAAT 625
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1. .55374
/note="assembly_fragment:00137
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-5E12"
                                                                                                                                                                                                                                                                                                                                                       Danio rerio (zebrafish)
Danio rerio
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                                                                                                                                                                                 Submitted (12-NOV-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA (bases 1 to 112917)
Shaulis, Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 TATAGTACAATCCAACCCTTTGAGAGGTTAATGTGTGTGCGGATTTTCTAGATAAACAAG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-JUN-2003) Department Of Chemistry And Blochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUN-2003) Department Of Chemistry And Blochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                  Submitted (06-JUN-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                   Submitted (08-MAR-2003) Department Of Chemistry And Blochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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Direct Submission
                                                                                                                                      Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D. and Roe, B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OK 73019, USA 6 (bases 1 to 112917)
Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A.
2 (bases 1 to 112917)
Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.
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On Jun 11, 2003 this sequence version replaced g1:31560173.
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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68.5%; Pred. No. 3.3e-06;
tive 1; Mismatches 69;
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/organism="Medicago truncatula"
/mol_type="genomic DNA"
/db_xref="taxon:3880"
/clone="mth2-30,23"
                                   Cook, D., Kim, D. and Roe, B.A. Direct Submission
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                                                                                                     OK 73019, USA
3 (bases 1 to 112917)
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Best Local Similarity 68.5°
Matches 152; Conservative
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RESULT 13

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182467
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Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 2 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC137839 147956 bp DNA 11near HTG 27-MAY-2003 Medicago truncatula clone mth2-34j11, WORKING DRAFT SEQUENCE, 18
                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 196490)
Hyman.R.W., Oin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Blact Submission
Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 TATTACGTTGATGGTAAAAAATAAATATATTTGTTACCATTTAAAAAGTCATAAATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 6.9%; Score 110.8; DB 2; Length 196490; Local Similarity 64.5%; Pred. No. 3.2e-06; es 182; Conservative 0; Mismatches 97; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 181303: contig of 181303 bp in length 181304 181503: gap of unknown length 181504 196490: contig of 14987 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="plasmodium falciparum"
/mol_type="genomic DNA"
/db_xref="taxon:5833"
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1. .196490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved
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AC137839/c
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110928 TCAGTTTCTAAAAAAAAAATACAGCATGGAAAACTCTGAAAAAACACAAAAACACAAAAACACTTTTC 110869
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Danio rerio clone CH211-77C11, *** SEQUENCING IN PROGRESS ***, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Opprinifornes; Cyprinidae; Danio.

( pases 1 to 195032)

Talbotyw.S., Rauch, G.J., Grimwood, J., Dickson, M., Schmutz, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 195032)
Talbot, W.S., Rauch, G.J., Grimwood, J., Dickson, M., Schmutz, J. and
                                                                                                                                                                                                                                                                                                                                    228 TCATAAATATAGTACAATCCAACCCTTTGAGAGGTTAATGTGTGCGGATTTTCTAGAT
                                                                                                                                                                                                                                                                                                                                                                                   288 AAACAAGGYGCCATTCACGATTCTTCTTGGTGCAGCTTGGAGAACCCTATCCTGGGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408 TTTTTTTCATCCTTCCTACCAAAAAAAAAAGTCATAAATATAGTTTATACATATAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 GAAGATTTACTTCTTGTTGATGCTTCTAGAGTACAGCTCCTTAAGGCTGTAGTCTAGTTT
                                                                                                                                                                                                                                                                                   Gaps
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Submitted (122-MAY-2003) Stanford Human Genome Center, 975
California Avenue, Palo Alto, CA 94304, USA
* NOTE: This is a "working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pleces
* is believed to be correct as given, bowever the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                  Length 147956;
                                                                                                                                                                                 /clone_lib="Medicago truncatula BAC library H2" 24438 c 25475 g 48056 t 1738 others
                                                                                                                                                                                                                                                                                 5;
95337: contig of 16654 bp in length 95437: gap of unknown length 121254: contig of 25817 bp in length 121354: gap of unknown length 147956: contig of 26602 bp in length:
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                                                                                                                                                                                                                                                 6.9%; Score 110.6; DB 2;
61.2%; Pred. No. 3.6e-06;
iive 1; Mismatches 120;
                                                                                               1. .147956
//organism="Medicago truncatula"
//nol_type="genomic DNA"
//lb_xref="taxon.3880"
/clone="mth2-34j11"
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HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
Danio rerio (zebrafish)
Danio rerio
                                                                                   Location/Qualifiers
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             95338
95438
121255
121355
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AC144827
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                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
                                                                                                                                                                                                                                                                                                             Submitted (04-DEC-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-MAY-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                            Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B. Cook, D., Kim, D. and Roe, B.A. Medicago truncatula BAC Clone mth2-34j11
                                                                                                                                                                                                                                            T (bases I to 147956)
Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.
Cook,D., Kim,D. and Roe,B.A.
                                                                                                                                                                                                                                                                                                                                           OK 73019, USA

3 (bases 1 to 147956)

Shaulls., Lin.S., Dixon.R., May.G., Sumner,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OK 73019, USA
ON MAY 27, 2003 this sequence version replaced gi:30270629.
Center: Department Of Chemistry And Biochemistry
The University of Oklahoma
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HTG; HTGS_PHASE]; HTGS_DRAFT.
Medicago truncatula (barrel medic)
Medicago truncatula
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The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center, funded by the NH Centers of Excellence in Genomic Science (CEGS) initiative (http://cegs.stanford.edu). The clone was isolated from the BAC library CHORI-211 (http://bacpac.chori.org).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 191969 bases at least Q40 Consensus quality: 192317 bases at least Q30 Consensus quality: 192756 bases at least Q30 Estimated insert size: 190000; agarose-fp estimation Estimated insert size: 193122; sum-of-contigs
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                This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 61516: contig of 61516 bp in length
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117922: contig of 56306 bp in length
118022: gap of unknown length
125177: contig of 7095 bp in length
126859: contig of 1642 bp in length
126859: contig of 1642 bp in length
134961: contig of 1642 bp in length
135061: gap of unknown length
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147553: contig of 12492 bp in length
147553: contig of 12492 bp in length
195032: contig of 47379 bp in length
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Alfalfa salt induc	Haematopoietic cel	Chemically treated	Human chemically p	Haematopoietic cel	Haematopoietic cel	Chemically treated	Human immune syste
		ΙΩ		AAZ34539	ABZ10246	ABL70376	ABK40038	ABZ10246	ABZ10100	ABL54336	ABL32315
		В	!	21	25	24	24	25	25	24	24
		Match Length DB ID		1612	8056	16258	16258	8056	8056	6641	6641
dP	Query	Match	1 1 1 1 1 1 1	88.5	7.1	6.2	6.2	6.2	5.9	5.8	8
		Score		1427	114	100.6	100.6	100.2	95.2	93.2	93.2
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RESULT 1 AAZ 34539 A	92.4 5.7 9770 24 ABL32032 Human immune 92 5.7 6621 24 ABL70156 Chemically t.	5.7 6621 .24 ABK33933 Human	5.7 6621 24 AAS61098	5.7 6621 25	5.7 6621 25 ABZ10130	92 5.7 6621 .25 ABZ10244	.6 5.7 11745 24 ABK28332	.4 5.7 6641 24 ABL32315	91 5.6 3991 22 AAD16633	.6 5.6 8056 25 ABZ10100	.0 5.0 8130 24 ABK3995/ 6 5 6 8136 24 ABK3955	5.6 11745 24 ABK28332	5.6 18060 24 ABL92212	90 5.6 18060 24 AAD22313	.4 5.5 6621 24 ABL/U156 4 5.5 6631 34 ABK33633	.4 5.5 6621 24 AAS61098	.4 5.5 6621 25 ABZ09984	.4 5.5 6621 25 ABZ10098	.4 5.5 6621 25 ABZ10130	.4 5.5 513445 22 AAI61373 Sovber	.2 5.5 8136 24 ABK39957	.2 5.5 8136 24 ABL32555	.2 5.5 3296 23 ABLI7264 Drosop	.4 5.4 14551 24	.2 5.4 8136 24 ABK39956 Human	.2 5.4 8136 24 ABL32554 Human	.2 5.4 14551 24 ABL34585 Human	.2 5.4 18855 24 8 5.4 (69739 24	.2 5.3 20420 22 AAK73165 Human	ALIGNMENTS		4539 standard: DNA; 1612 BP.	4539;	•	EB-2000 (first entry)	lfa salt inducible MsPRP2 gene promoter region.	gene; promoter; Alfinl; transcription	tolerance; stress tolerance; transgenic plant; root; ds	Medicago sativa.	Lycation/Qualif	ein_bind complement (7187	/note= "Alfin1	complement (77	/note= "Alfinl b	d complement (10
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                                                                                                                                                                                                                                                                                                                                                                         This is the nucleotide sequence of the promoter region of the root directed salt-inducible MSPRP2 gene of alfalfa. The promoter includes potential sites for binding to Alfini (see AAY3143), a newly identified root-specific transcription factor of alfalfa that is associated with salt tolerance. The full or partial MSPRP2 promoter sequence can be used by itself or in conjunction with other promoter sequence elements to construct new composite promoter regulatory sequences that would give root-specific and/or him protein regulated expression to other genes transferred into plants. The Alfini protein binding sequences could also be used, as concatenates or in conjunction with other promoter regulatory sequences it is believed the introduction of Alfini binding states in appropriate promoter could lead to regulatory sites in appropriate promoter could lead to regulation of additional genes by Alfini. The invention may be used to
                                                                                                                                                                                                                                                                                                                    Producing novel transgenic plants tolerant to a wide variety of biotic and ablotic stress conditions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 TAATGTGTGCGCGATTTTCTAGATAAACAAGGTGCCATTCACGATTCTTCTTGGTGCAG
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                                                                                                                   of coding sequence"
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Pred. No. 1.4e-178;
1; Mismatches 21;
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94.8%;
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Matches 1509; Conservative
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  protein_bind
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                                                                                                                                                                                                                                   The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least I gene and/or their regulatory regions in a associated with at least I gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least I reagent, which distinguishes between methylated and non-methylated CpG dinclectics within the target nucleic acid. ABZ09661 to ABZ18118 crepresent specifically claimed nucleotide sequences from the present invention. Oligonuclectides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder hematopoietic cells; for differentiating between acute inymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder
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1342 CAATTTGCAGTATTATGATTTAGATTGCTGCTAATACGGTCCGTGAATGTGATCACT 1401
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                                         1402 CACGAGAAAGAGGTATCAAAATTTCAAGGTATTTTTATTTTTTTAACAAATAAAATTTC
                                                                                                                                                                                                           TCATAGTACACTACATTCTTTGAAACATGGCTAACTATGCTCTAGCCAATGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 '. Braun A, Distler J, Guetig D, Howe A, Mueller J; Plepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E; Lipscher E, Maier S, Model F, Mueller V, Otto T; Schwope I, Ziebarth H;
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                                                                                                                                                                                                                                                                                                                                                              9
related sequences and their complements; and as primers for the amplification of heematopoletic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of mamearopoletic call proliferative disorders. The present method enables a highly specific classification of hemantopoletic cell proliferative disorders allowing for improved and informed treatment of patients.
                                                                                                                                                                                                                                                                                                                                                                                                              301 TICACGAITCTICTIGGIGCAGCTIGGAGAACCCTAICCIGGGCTIGGAAGAITTACTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1318 ITTTTTATAATTTAATTTTTAAAAAAATATTACATTTTTATATATTAATATTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1198 ITAAAATTITAAAATTAATTAATAATCAAAAATATATTAATTTTAAATTTTCAAATA
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                                                                                                                                                                                                                                                                                                                                                                 1 TTTTATANATATTTAAGCCTTGATAATAATTTTGCGATCTATATATAAGCCCCACTACCAAT
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                                                                                                                                                                                                                                                               Length 8056;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                    Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 other;
                                                                                                                                                                                                                                                                  Score 114; DB 25;
Pred. No. 5.7e-07;
1; Mismatches 751;
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Local Similarity 44.6%;
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with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations, as well as method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL/0111-ABL/0656 represent chemically pre-treated genomic DNA's of genes associated with cell signalling.

Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATATATATATATATATATAATAATTTTATTTTACCAATTTAAAATTATATATATATA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1723 CCAAAACTCCTTACAAATACTACTTCAAAAATTCACTCCACCCCATCTAAAACCCCAT 1664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 AAAGTCATAAATATAGTTTATACATATAACTTTAATAAAATAAAAATTTCATCCCTA 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATATAATTTGTTACCATTTAAAAGTCATAAATATAGTACA-ATCCAACCCTTTGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                 Sequence 16258 BP; 4242 A; 330 C; 3801 G; 7885 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                           Score 100.6; DB 24; _____
Pred. No. 2.9e-05; _______
..._matches 389; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           6.2%;
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Best Local Similarity 49.0
Matches 381; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid comprising a sequence of at led 18 bases of a segment of chemically pretreated DNA of genes associated
                                                   AAGGATGCATGATTCGATTACAAAAACAAAATACTAATAATTCTAGCACAAAGTTTAAAG
                                                                                             CTTTCATCACGGGTCTAACAGCACCACTTGTCACTACATGTCAAAAATGTCCTCTAGTAC
                                                                                                                                                                                                                                                                                                                                                                    Chemically treated cell signalling DNA sequence complementary to#133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; cytosine methylation; cell signalling disease; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 266; 24pp+sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL70376 standard;
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1723 CCAAAACTCCTTACAAATACTACTTCAAAAATTCACTCCACCCCATCTAAAACCCCAT 1664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1663 AACAAAACMAAAATAATCATTATTTCTCTCCCTTTCTAACTCCTCACTTACCTCTCT 1607
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                           AAATATAA TTTGTTACCATTTAAAAGTCATAAATATAGTACA - ATCCAACCCTTTGAGAG
                                                                                                                                                                                                                                                                                                                437 AAAGTCATAAATATAGTTTATACATATAACTTTAATAAAAATAAAAATTTCATCCCTA
    TATATATATATATATATATAATATTTTTTTTTACCAATTTAAAATTATATATATAT
                                                                                             2263 TATACATATATAAAAATAAAATATATATATATATATAAAAATAT
                                                                                                                                                                                                                                                                                    261 GTTAATGTGTGCGGATTTTCTAGATAACAAGGYGCCATTCACGATTCTTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                321 AGCTTGGA3AACCCTATCCTGGGCTTGGAAGATTTACTTCTTGTTGATGCTTCTAGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           497 AAAACATASTAGAAATTTCATAAAAAAATAT-TGTTTATAATTTACATGCCGTTACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                616 ACTAAAAAATAATTTCTCTCCTGATTTATATGAAATGACATTTTTTTGGAACATGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haematopoietic cell proliferation disorder related DNA sequence #386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from 87 sequences and their complements. The chemical pretreatment is bisulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. Also included are an oligomer (II) in particular an oligomucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is identical to a chemically pretreated DNA of genes associated with pharmacogenomics and their complements, arranged in an array for analysing diseases associated with the methylation state (CPG) and/or detecting SNPS (single nucleotide polymorphisms) of the 87 sequences. The oligomers may also be used as PCR primers and therapy of solid tumnours and cancer. The present sequence represents one the 87 DNA sequences or its complements is useful for diagnosis necessars one the 87 DNA sequences or its complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDHE (NM_000693), CYP11A (NM_000781), CYP11B1 (NM_001979), CYP3A3 (NM_00776 and NM_017460), DPYD (NM_0001910), EPHX2 (NM_001999), OCLM (NM_012980), NM_019900, NM_019901, NM_019902, NM_019903, NM_019909), NM_019999) and their complementary sequences, or a sequence (S1) chosen
                                                                                                                                                                                                                              Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16258 BP; 4242 A; 330 C; 3801 G; 7885 T; 0 other;
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                                                                                                                                                                                      Human chemically pretreated gene sequence #60 strand 2.
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Pred. No. 2.9e-05;
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                                          ABK40038 standard; DNA; 16258 BP
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Similarity 49.08;
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01-SEP-2000; 2000DE-1043826.
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G, Lesche R, Leu E;
Mueller V, Otto T;
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Lewin A, I
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                                                                                                                                                              Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Braun A, Distler J, Guetig D, Howe A, Mueller J; Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E; Lipscher E, Maier S, Model F, Mueller V, Otto T; Schwope I, Ziebarth H;
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                                                                                                                                                                                                                                               Claim 28; SEQ ID 386; 117pp; English
              (EPIG-) EPIGENOMICS AG.
                                                                                                                                WPI; 2003-018942/01
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Pelet C,
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                                                                                                                          The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a blological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between acute disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single related sequences and their complements; and as primers for the polymorphisms (SNPs) of haematopoietic cell proliferation disorder related may be used for detecting a predisposition to, differentiation between also be used for detecting a predisposition to, differentiation between subjects cell proliferation of haematopoietic cell proliferation denables a highly specific classification of haematopoietic cell proliferative disorder. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients.
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                           Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTACGTTGATGGTAAAAAAAATATATTTTTTGTTACCATTTAAAAGTCATAAATATAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 25; Length 8056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 95.2; DB 25; Length Pred. No. 0.00016;
1; Mismatches 679; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 other;
                                                                                                   Claim 28; SEQ ID 240; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.98;
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Matches 551; Conservative
WPI; 2003-018942/01
                                                                         dinucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGGATCCATGATTCGATTACAAAAACAAAATACTAATAATTCTAGCACAAAGTTTAAA
                                                     1318 TTTTTTARATTTATAATTTTAAAAAATATTACGTTTTTATATATATAATTACG
                                                                                                                                                                                                                                                                                                                                         ATGAATATATATTTTGGGCGATCAAACACAAGAATCATTACGATAACATGCTTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATAAAAACATCAAAAGTCTAGCAAAATGTTTTTTGCGATGACACATTTCATATAGTTT
                                                                                                            TTCATTG(;TTAAAAAACTAAAAATAATTTCTCTCCTGATTTATATGAAATGACATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      780 ACCCCGTCAATCTTCTTTTTTTACCCAATAAACATTGAAATGTTGCTTCTTTCGTTAAG
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neurodegenerative disorder; Herpes simplex virus; renal ischaemia;
amyotrophic lateral sclerosis; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemically treated apoptosis gene complementary to gene #18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1200 TATTGATCAAATTTGGCTATGAATTCAAAAAAATTCA 1239
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CITCITITITITACCCAATAAACAITGAAAIGTIGCITCITITCGITAAGCAIAAAAACAI 850
                                                                                                                                                                                                                                                                                                                                                                 GATTCGATTACAAAAACAAAATACTAATAATTCTAGCACAAAGTTTAAAAGCAATATTATA 970
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                                       2934 AATGTAATATTTTTATGTATTTTTTGGATTAAAAATGAATTTATATAAAGTAATGAT
                                                                           671 AAGGGTATTGATTTTACCACCTTTTACACCTTTCAAAGCCATTCAAGGATGAATATAGA
                                                                                                                                               CAAAGTCTAGCAAAATGTTTTTTGCGATGACACATTTCATATAGTTTAAAGGATGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antilnflammatory; cancer disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzhelmer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 288; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 288.
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                    This invention relates to chemically pre-treated DNA of genes associated with apoptosis. The nucleic acids are used to allocate patients for specific therapy for HIV infection, Bloom syndrome, cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours and cancers. This nucleotide sequence represents a chemically treated apoptosis gene. Even SEQ ID numbers are the complementary DNA strands to the odd SEQ ID numbers. The sequence data for this patent is not represented in the printed specification but is based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 TITAAGCTIGATAATATITIGCGATCTATATATA-AGCCCACTACCAATTTAAAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTTTGAGAGGTTAATGTGTGTGCGGATTTTCTAGATAAACAAGGYGCCATTCACGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTTGGTGCAGCTTGGAGAACCCTATCCTGGGCTTGGAAGATTTACTTCTTGTTGATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 TCCCTAAAAACATAGTAGAAATTTCATAAAAAAAATATTGTTTATAATTTACATGCCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for diagnosis of associated diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6641 BP; 2495 A; 22 C; 984 G; 3140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      information supplied by the European patent office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93.2; DB 24;
Pred. No. 0.00031;
0; Mismatches 503;
                                                                                                                                                                                                                                                    Claim 1; Seq ID #36; 24pp; English.
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                                                                                                             Berlin
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 46.5%;
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                                                                                                           Piepenbrock C,
                                                                         (EPIG-) EPIGENOMICS AG
                                                                                                                                               WPI; 2002-017444/02.
                30-JUN-2000;
01-SEP-2000;
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                               (first entry)
                                                               3294 TATTTTATTA 3303
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                                           971 AAGCTTCATA
                                                                                                                    ABL32032 standard;
                                                                                                                                                                                                                                                                                                                           WO200200928-A2
                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610
                                                                                                                                                                                                                           including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                              2646 TTAATATAAAGAGATATGATTTAAGTTAGGTTGTATGTGGAAAAGTTAGATATTTTT----T
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                                                                                                                                                                                 191 GGTAAAAAATAAATATATTTGTTACCATTTAAAAGTCATAAATATAGTACAATCCAAC
                                                                                                                                                                                                                                                                                                               251 CCTTTGAGAGGTTAATGTGTGTGCGGATTTTCTAGATAAACAAGGYGCCATTCACGATTC
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 system disorders
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                                                                                                                                                                                                                                                                                                                                                                                                   491 TCCCTAAAAACATAGTAGAAATTTCATAAAAAAATATTGTTTATAATTTACATGCCGTT
                                                                                                                    Gaps
                                                                                                                    16;
                                                                                               6641;
                                                    diseases. The present sequence is a gene of the invention
                                                                                              Score 93.2; DB 24; Length Pred. No. 0.00031;
                                                                                                                    Indels
                                                                        Sequence 6641 BP; 2495 A; 22 C; 984 G; 3140 T; 0 other;
 treatment of immune
                                                                                                                    503;
                                                                                                                   0; Mismatches
can be used in the diagnosis and
                                                                                               Match 5.8%;
Local Similarity 46.5%;
                                                                                                                   451; Conservative
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                                                                  1150 TATCTAAA;CCATCTTTCTTAAATAACTTTCAAACTCCCAATTTTAAAATTAAATATA 1091
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911 GATTCGATTACAAAAACAAAATACTAATAATTCTAGCACAAAGTTTAAAGCAATATTATA 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TATAAATAFTTAAGCTTGATAATAATTTTGCGATCTATATATAAGCCCACTACCAATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarteriosclerctic; antianaemic; oytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiantinflammatory; cancer, eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 5; 32pp + Sequence Listing; German.
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Best Local Similarity 61.0%; Pred. No. 0.00037
Matches 150; Conservative 0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated gene SEQ ID
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as expostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL7011-ABL70626 represent chemically pre-treated with cell signalling.
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                                                                                                                                                  243
   Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling
                                                                                                                                               184 CGTTGATGGTAAAAAAAATATATATTTTGTTACCATTTAAAAGTCATAAATATAGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemically treated cell signalling DNA sequence complementary to#23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell signalling; cytosine methylation; cell signalling disease; cancer; tumour; cytostatic; ds.
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                              244 ATCCAA 249
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The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic DNA which has any one of the sequences of (ABMS4012) or its complement. Also included are an oligonucleotide or peptide nucleic acid (or set thereof) of at least 9 nucleotides which hybridises to (I), probes for detecting cytosine methylation or single.

Complement SNP) in (I), an array of oligomers or peptide nucleic acids for analysing diseases associated with the nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide nucleic acids for analysing diseases associated with the complement of the CpG dinucleotides of (I). The array is useful to determining genetic and/or epigenetic parameters, classification, differentiation, grading, treatment and/or diagnosis of astrocytomas yor the predisposition to astrocytomas by analysing cytosine methylations, involves obtaining a biological sample containing genomic DNA, extracting the genomic DNA, converting cytosine bases which are unmethylated at the 5-position, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour, by chemical treatment and amplifying chemically pre-treated genomic DNA fragments using the array and a polymerase, where the
                                                                                                                                                          5068
                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ds; astrocytoma; cytostatic; staging; cysteine methylation; CpG; bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry; matrix assisted laser desorption/lonization mass spectrometry.
                                                                                                                                                                                                                           182 TACGTTGATGGTAAAAAAATATAATTTGTTACCATTTAAAAGTCATAAATAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA for staging of Astrocytomas, complement, #8.
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                                                                                                                                                                                                                                                                                                                                       ABK33933 standard; DNA; 6621 BP.
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01-SEP-2000; 2000DE-1043826.
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Conservative

Similarity

Best Local Simi Matches 146;

Query Match

5.7%; Score 92; DB 24; Length 6621; 61.9%; Pred. No. 0.00044;

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2000DE-1019173
  07-APR-2000;
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                                                                                                                                                                                                                                                                                                           disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying methylation status of one or more cytosine positions, and analysing methylation status of the cytosine positions by reference to one or more data sets. The genomic DNA is chemically treated by using a bisulphite, hydrogen sulphite or disulphite. The amplification step amplifies DNA which is of particular interest in astrocytoma or brain tissue, based on the specific genomic methylation status of brain tissue, as opposed to background DNA. The amplificates carry a fluorescent label or radionuclide. Optionally, the labels of the amplificates are detachable molecule fragments having a typical mass which are detected in a mass spectrometer. The fragments of chemically pre-treated genomic DNA to be amplified, have a single positive or negative charge for a better detectability in the mass spectrometer. Preferably, the amplificates are detected by matrix assisted laser desorption/ionization mass spectrometry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4889 IGTGTGTATATATATATATATATATATATATGTGTATATATATATATATATATATATATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic
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    182 TACGTTGATGGTAAAAAAAATAAATTTGTTACCATTTAAAAGTCATAAATAT 237

                                                                                                                                                                                                                                                                                                                                                (MALDI) or using electron spray mass spectrometry (ESI). The present sequence is one of the chemically pre-treated reference DNA samples of the invention.
amplificates carry a detectable label. The method further involves
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24; Length 6621; 0.00044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene regulation-associated gene oligonucleotide #53.
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; Pred. No. 0.0004
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     directly from WIPO at
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Matches 146; Conservative
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The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 91 kmon genes (or complementary sequences). The chemical pretreathent converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The bNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, heamophilia, soild tumours and cancer, Werner syndrome, sethma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4889 TGTGTGTATATATATATATATATATATATGTGTATATATATATATATATATATATATATG 4948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ITTATAAANATITAAGCITGATAATAITITGCGATCIATATATAAGCCCACTACCAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; haematopoietic cell proliferation disorder; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6621;
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61.9%; Pred. No. 0.00044;
Live 0; Mismatches 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 54; 26pp; English.
                                                                                                                                                                                                Berlin K;
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30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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Best Local Similarity 61.99
Matches 146; Consenvative
                                                                                                                                                                                            Olek A, Piepenbrock C,
                                                                                                                  (EPIG-) EPIGENOMICS AG.
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us-09-647-841b-1.rng

Haematopoietic cell proliferation disorder related DNA sequence #238.

BP.

ABZ10098 standard; DNA; 6621

RESULT 14

4BZ10098

16-JAN-2003 (first entry)

ABZ10098;

Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

cytosine methylation state; gene; ds

26-MAR-2002; 2002WO-EP03401. 26-MAR-2001; 2001US-278333P.

WO200277272-A2.

03-OCT-2002.

Homo sapiens

(EPIG-) EPIGENOMICS AG.

Berlin K, Lewin A, Pelet C,

olek A,

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The present invention describes a method for detecting and differentiating between haematopoletic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a bological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ0861 to ABZ1881 crepresent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoletic cells and proliferative disorder haematopoletic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoletic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoletic cell proliferation disorder related sequences. The uncleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoletic cell proliferative disposition of haematopoletic cell proliferative disposition to, differentiation disorder.
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    acute myelogenous leukaemia;
                                                                                                                                                                                                                                                                                                                                    Mueller J;
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Best Local Similarity 61.9%; Pred. No. 0.00044;
Matches 146; Conservative 0; Mismatches 90
gene therapy; lymphocytic leukaemia; cytosine methylation state; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 28; SEQ ID 124; 117pp; English
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                                                                                                                                                                                                    26-MAR-2002; 2002WO-EP03401.
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                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
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                                                                                                           WO200277272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dinucleotides
                                                                   Homo sapiens
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Detecting and differentiating between hematopoietic cell proliferative

WPI; 2003-018942/01.

Howe A, Mueller J; G, Lesche R, Leu E; Mueller V, Otto T;

, Braun A, Distler J, Guetig D, Plepenbrock C, Adorjan P, Grabs Lipscher E, Maier S, Model F, Schwope I, Zlebarth H;

disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CPG

Claim 28; SEQ ID 238; 117pp; English.

dinucleotides

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differentiating decided as a mechanical proliferating and associated with at least 1 gene and/or their regulatory regions in a sociated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonocleotides from the present invention can be used: for differentiating between healthy haematopoictic cells and proliferative disorder haematopotetic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytcosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related myelogenoes from the present invention can also be used for detecting a predisposition to, differentiating of haematopoietic cell proliferation between some also be used for detecting a predisposition to, differentiating of haematopoietic cell proliferation between also be used for detecting a predisposition to, differentiating of haematopoietic cell proliferation of haematopoietic cell pro
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182 TACGTTGATGGTAAAAAATAAATATAATTTGTTACCATTTAAAAAGTCATAAATAT 237

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4889 TGTGTGTATATATATATATATATATATATGTGTATATATATATATATATATATATATATAT
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                                 Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                              182 TACGTTGATGGTAAAAAAAATAATATTTGTTACCATTTAAAAGTCATAAATAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                  Haematopoietic cell proliferation disorder related DNA sequence #270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; haematopoletic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ., Braun A, Distler J, Guetig D, Howe A, Mueller J; Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E; Lipscher E, Maier S, Model F, Mueller V, Otto T; Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes a method for detecting and
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Pelet C,
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subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoletic ceil proliferative disorders. The present method enables a highly specific classification of haematopoletic cell proliferative disorders allowing for improved and informed treatment of patients.
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                                                                                                                                                                                                                  Gaps
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                                                                                                                                                              Query Match 5.7%; Score 92; DB 25; Length 6621; Best Local Similarity 61.9%; Pred. No. 0.00044; Matches 146; Conse.vative 0; Mismatches 90; Indels
                                                                                                                 Sequence 6621 BP; 1770 A; 0 C; 1781 G; 3070 T; 0 other;
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Search completed: August 14, 2003, 19:03:51 Job time : 489 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

August 14, 2003, 16:53:44; Search time 112 Seconds (without alignments) 6356.705 Million cell updates/sec Run on:

US-09-647-841B-1

1613 1 tittataaatatttaagctt......tgaacttgagtaccttactc 1613 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

569978 segs, 220691566 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* Issued_Patents_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	lt 5. Score	Ouery Match	Length	DB	ID	Description
	1 80	0 5.0	53332	7	US-09-801-861-3	Sequence 3, Appli
υ	2 75.(6 4.7	53332	4	US-09-801-861-3	'n
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	5	3 4.5	1001	4	US-09-671-317-141	141
	6 72.8	8 4.5	5340	4	US-09-627-122-21	21,
ပ	7 7	1 4.4	6152	٣	US-08-973-462-1	1,
	8 70.8	8 4.4	19124	7	US-08-487-826B-13	13
	9 70.4	4 4.4	6265	4	US-09-129-112-3	3,
Ö	10 69.4	4 4.3	1001	4	US-09-671-317-141	141
Ö	11 69.4	4 4.3	319608	4	US-09-539-333D-1	1,
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• •	14 69	9 4.3	1890	9	5312912-3	Patent No. 5312912
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ပ	18 68.6	6 4.3	5340	4	US-09-627-122-21	21,
	19 68.3	2 4.2	8920	~	US-08-446-855A-1	7,
	9	4	8920	٣	US-09-150-741-1	7
υ	21 68	8 4.2	1890	ø	5312912-3	Patent No. 5312912
o	22 67.(4	6124	4	US-08-213-419B-3	'n
. •		2 4.2	6152	m	US-08-973-462-1	Ļ
υ		6 4.1	2663	7	US-08-136-743B-3	'n
	25 66.2	2 4.1	6038	m	US-09-305-639-4	Sequence 4, Appli
	26 66.2	2 4.1	6038	4	US-09-525-160B-2	~
,	27 66	2 4.1	7622	m	US-09-305-639-1	Sequence 1, Appli

Sequence 1, Appli	Sequence 1, Appli	Sequence 8, Appli	8,	Sequence 8, Appli	Sequence 8, Appli	Sequence 186, App	Sequence 2, Appli	Sequence 13, Appl	Sequence 186, App	Sequence 4, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 55, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appli
US-09-525-160B-1	US-09-426-290-1	US-07-991-867B-8	US-08-107-755A-8	US-08-544-332-8	US-09-370-861A-8	US-08-998-416-186	US-07-867-106-2	US-08-487-826B-13	US-08-998-416-186	US-09-078-294-4	US-09-078-294-3	US-08-213-419B-3	US-09-522-217-55	US-09-801-876B-3	US-08-947-823-1	US-09-078-294-3	US-09-539-333D-1
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7622	168575	1511	1511	1511	1511	615	5852	19124	615	80246	80595	6124	3072	148567	51952	80595	319608
4.1	4.1	4.1	4.1	4.1	4.1	4.0	4.0	4.0	4.0	4.0	4.0	4.0	3.9	3.9	3.9	3.9	3.9
66.2	65.8	9.59	9:59	9.59	9.69	65.2	65.2	64.4	64	64	64	63.8	63.6	62.8	62.4	62.4	62.4
28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: C1001098
CURRENT APPLICATION NUMBER: US/09/801,861
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3. Application US/09801861
Patent No. 6492154
GENERAL INFORMATION:
APPLICANT: YAN, Chinhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
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                                                                                                                                                                                                                                                                                                                                                         Length 53332;
                                                                                                                                                                                                                                                                                                                                                     5.0%; Score 80; DB 4; Length 533
60.6%; Pred. No. 1.4e-06;
tive 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31636 TITITATATATATATATGTATTTTTTTTTTTGA 31671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TTACGTTGATGGTAAAAAAAATAAATATATTGTTA 216
             Sequence 3, Application US/09801861
Patent No. 6492154
                                                                                                                                                                                                                                                                                                                                                       Query Match 5.0°
Best Local Similarity 60.6°
Matches 131; Conservative
                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Human
US-09-801-861-3
                                                                                                                                                                                                                                                             53332
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US-09-801-861-3
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us-09-647-841b-1.rni

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Sequence 141, Application US/09671317
Patent No. 6528260
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chom, Annick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLIS
FILE REPERENCE: 62.03.CIP
CURRENT APPLICATION NUMBER: US/09/671,317
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PS 9/536,178
PRIOR PRILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT/IB00/00403
     1098 TATACATATATAAATATACATATATAAATATATATACATATATAAATATATAAATATACA 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TTACGTTGATGGTAAAAAAATAAATATTTGTTACCATTTAAAAGTCATAAATATAGT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6%; Score 73.8; DB 4; Length 15418; 60.2%; Pred. No. 1.7e-05; tive 0; Mismatches 102; Indels 2;
                                                                                                                                                                                                                                          APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Geld, Joseph
APPLICANT: Lebkowski, Jane
TITLE OF INVENTION: Tpacked stem cells
FILE REFERENCE: 096/003
CURRENT APPLICATION NUMBER: US/09/783,203
CURRENT APPLICATION NUMBER: 60/253,443
PRIOR APPLICATION NUMBER: 60/253,443
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
FEMALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ACAATCCAACCCTTTGAGAGG 261
                                                                                                                                                                                          ; Sequence 1, Application US/09783203; Patent No. 6576464; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.6
Best Local Similarity 60.2
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 15418
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31436 ATAAAAATATAAAATATAAAATATATACAAATATATAAATATATAAATATATAAAA 31377
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                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                        Query Match 4.7%; Score 75.6; DB 4; Length 5:
Best Local Similarity 57.0%; Pred. No. 9.2e-06;
Matches 138; Conservative 0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 8.4e-06;
0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1. Application US/09783203
Patent No. 6576464
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gold, Joseph
APPLICANT: Lebkowski, Jane
TILE OF INVENTION: Tpacked stem cells
FILE REFERENCE: 096/003
CURRENT APPLICATION NUMBER: 06/253, 443
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
WUMBER OF SEQ ID NOS: 7
                                                                            FastSEQ for Windows Version 4.0
FILE REFERENCE: CL001098
CURRENT APPLICATION NUMBER: US/09/801,861
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
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Best Local Similarity 57.4%;
Matches 136; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1
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                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-09-801-861-3
                                                                                          SEQ ID NO 3
LENGTH: 53332
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US-09-783-203-1/c
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GENERAL INFORMATION:
APPLICANT: DRUILHE, PIERRE
APPLICANT: DRUILHE, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
TITLE REPERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: 05/08/973,462B
CURRENT APPLICATION NUMBER: PCT/FF96/00894
EARLIER APPLICATION NUMBER: PCT/FF96/00894
EARLIER APPLICATION NUMBER: F 95/07007
EARLIER APPLICATION NUMBER: F 95/07007
EARLIER PILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                        0;
                                         Length 5340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.4%; Score 71; DB 3; Length 6152; 62.1%; Pred. No. 5e-05;
                                                                        Indels
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                                     Score 72.8; DB 4;
Pred. No. 2.2e-05;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5651 ATTAATTTATTGTTCGCTCCAATCATTCA 5621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 GTCATAAATATAGTACAATCCAACCCTTTGA 257
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GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08973462B Patent No. 6191270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chitnis, Chetan
Miller, Louis H.
Peterson, David S
Su, Xin-zhaun
                                     Query Match 4.5%;
Best Local Similarity 72.0%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                         4789 ATTTATATTAT 4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62.1
Matches 131; Conservative
                                                                                                                                                                                                                                                179 TATTACGITGAT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: P. falc::parum
US-08-973-462-1
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APPLICANT:
APPLICANT:
APPLICANT:
     US-09-627-122-21
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APPLICANT: Uhlmann, Eugen
APPLICANT: Uhlmann, Eugen
APPLICANT: Gethe, Gislinde
APPLICANT: Gothe, Gislinde
APPLICANT: Schwerdel, Marc
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 02481.1678
CURRENT APPLICATION NUMBER: US/09/627,122
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 21
LENGTH: 5340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                 PERTURE:

NAME/KEY: allele

LOCATION: 501

COTHER INFORMATION: 10-436-43: polymorphic base G or C

NAME/KEY: misc_binding

LOCATION: 482.500

OTHER INFORMATION: 10-436-43.mis1

NAME/KEY: misc_binding

LOCATION: 502.51

OTHER INFORMATION: 10-436-43.mis2, potential complement

NAME/KEY: primer_bind

COCATION: 502.51

OTHER INFORMATION: upstream amplification primer

NAME/KEY: primer_bind

COCATION: 859.878

OTHER INFORMATION: downstream amplification primer, complement

NAME/KEY: misc_binding

LOCATION: 489.513

OTHER INFORMATION: 10-436-43 potential probe

NAME/KEY: misc_binding

LOCATION: 297.539, 659, 650, 976.1001

OTHER INFORMATION: n-a, g, c or t

US-09-671-317-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.5%; Score 73; DB 4; Length 1001; Best Local Similarity 64.5%; Pred. No. 1.6e-05; Matches 109; Conservative 0; Mismatches 60; Indels
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SOFWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Plasmodium falciparum
                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-627-122-21
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Query Match 4.4%;
Best Local Similarity 57.1%;
Matches 128; Conservative
                                                                                                              ORGANISM: Dolichos biflorus
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: intron
LOCATION: (1617)..(1697)
                                                                                                                                                                                                                                                                                  (1023)..(1151)
                                                                                                                                                                                                                                                                                                                               (1152)..(1559)
                                                                                                                                                                                                                       intron
(945)..(1022)
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                                                                                                                                                                                                   (633)..(944)
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ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-671-317-141/C
                                                                   6265
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                          SOFTWARE: 1
SEQ ID NO 3
                                                                                            TYPE: DNA
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APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
CORRESPONDENCE: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3562 ТТАТАТТТТТТАТАССТТGGATTСТТАСАТТGTTTTATTATTATGATTATTAATTA 3621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ELZIEC. Marilynn E.
APPLICANT: BLISE. Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-0798108.
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT APPLICATION NUMBER: US 08/907,226
PRIOR APPLICATION NUMBER: US 08/907,226
PRIOR FILING DATE: 1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TITIATAAATATITAAGCITGATAATATITIGCGATCTATATATAAGCCCACTACCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19124;
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CAPPTER PASONEL FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: END PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Baselsen, Ned
REFERENCE/DOCKET NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 131-101CP1
TELECOMMUTCATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.4%; Score 70.8; DB 2;
Best Local Similarity 61.9%; Pred. No. 6.4e-05;
Matches 130; Conservative 0; Mismatches 77;
                                                                                                       ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach Center Drive 16th Floor CATAE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3739 TATTAGTGATGATTATAATAACCTATT 3768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TTACGTTGATGGTAAAAAAAATATAAT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09129112
Patent No. 6465716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 1in
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-129-112-3
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NAME/KEY: misc_feature
LOCATION: 31.1107
OTHER INFORMATION: 5'regulatory region g35018 gene
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LOCATION: 65854..67854
OTHER INFORMATION: 3'regulatory region g35018 gene
PRIOR APPLICATION NUMBER: US 60/162,288
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/416,384
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 231
SEQ ID NO 1
LENGTH. 319608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 18778...18862
OTHER INFORMATION: exon Bbis 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION: exon A 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: exon B 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: exon D g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION: exon E 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 64666..64812
OTHER INFORMATION: exon F 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: exon G g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: exon S 935030 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: exon T 935030 gene
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OTHER INFORMATION: exon U 935030 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 216836...316915
OTHER INFORMATION: exon V g35030 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: exon C g35018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: exon q35017
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LOCATION: 213818..215818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 201188..201234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 214676..214793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 25593..35740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 29388..:9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 29967..30282
OTHER INFORMATION: exor
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LOCATION: 14877..14920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 94124..94964
                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65505..65853
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
FOCATION: 1108..1289
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TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REPREBENCE: GRNEY: 04705
CURRENT APPLICATION NUMBER: US/09/539,333D
CURRENT FILING DATE: 2000-03-30
PRIOR PAPLICATION NUMBER: US 60/126,903
PRIOR PAPLICATION NUMBER: US 60/131,971
PRIOR PAPLICATION NUMBER: US 60/131,971
PRIOR PELING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR PELING DATE: 1999-04-30
PRIOR PELING DATE: 1999-04-30
PRIOR PELING DATE: 1999-07-14
PRIOR PELING DATE: 1999-07-14
PRIOR PELING DATE: 1999-07-14
PRIOR PELING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR PELING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/145,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AATATATGTATATATATATATATATTATTATTAAATATATGTATTA-ATGTTTT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                               THEN INCRMANION: 10-436-43: POLYMOLPHIC DASE GOIC CONTENT MANEKEY: misc_binding LOCATION: 482..500

JOTHER INCRMANION: 10-436-43.misl
LOCATION: 502..521

JOCHER INCRMANION: 10-436-43.misl, potential complement LOCATION: 502..521

JOCHER INCRMANION: upstream amplification primer NAME/EE; primer_bind LOCATION: 859..476

JOCHER INCRMANION: downstream amplification primer, complement NAME/EE; misc_binding LOCATION: 899..513

JOCHER INCRMANION: 10-436-43 potential probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69.4; DB 4; Length 10
Pred. No. 7.7e-05;
O' Wismatches 76; Indels
                              LOCATION: 501
OTHER INFORMATION: 10-436-43 : polymorphic base G or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.3%; Score 69.4; D
Best Local Similarity 62.1%; Pred. No. 7.7e
Matches 126; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,452
PRIOR FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 ACCATTTAAAAGTCATAAATATA 238
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Patent No. 6476208
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelert, Lydie
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

: LOCATION: 297,539,629,650,976.:1001

: OTHER INFORMATION: n-a, g, c or t

US-09-671-317-141
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US-09-539-333D-1/c
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us-09-647-841b-1.rni

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NAME/KEY: exon
LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene
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LOCATION: 240528..240617
OTHER INFORMATION: exon M1069 complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement 934872 gene
                                                                                                                                                                                                                                                      LOCATION: 216661..216952
OTHER INFORMATION: exon Qbis complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement 934872 gene
                                                                                                                                                                                     INFORMATION: exon Rbis complement 934872 gene
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LOCATION: 240528..240644
OTHER INFORMATION: exon MS2 complement g34872 gene
OTHER INFORMATION: 3'regulatory region g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 231870..231879
OTHER INFORMATION: exon 01 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 239719..239807
OTHER INFORMATION: exon N2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: exon 02 complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement g34872 gene
                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement g34872 gene
                                                                                         OTHER INFORMATION: exon R complement 934872 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 217027..217061
OTHER INFORMATION: exon Q1
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TOCATION: 239719..239853
                                          NAME/KEY: exon
LOCATION: 215819..215941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 230408..230721
                                                                                                                                                            215819..215975
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LOCATION: 23178
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APPLICANT: Cohen, Daniel
APPLICANT: Chen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, IIya
APPLICANT: Chumakov, IIya
APPLICANT: Bouqueleret, Iyale
APPLICANT: SCHIZOPHRENIA ASSOCIATED GENE, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: 53.0515.CIP
CURRENT APPLICATION NUMBER: US/09/679,409
PRIOR APPLICATION NUMBER: 09/539,333
PRIOR APPLICATION NUMBER: 09/416,384
PRIOR PLING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 TATTACGTTGATGGTAAAAAATAAATATAATTTGTTACCATTTAAAAGTCATAAAATATA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 GTACAATCCAACCCTTTGAGAGGTTAATGTGTGTGCGGATTTTCTAGATAAACAAGGYGC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3%; Score 69.4; DB 4; Length 319608; 58.4%; Pred. No. 0.00017; tive 1; Mismatches 92; Indels 8;
                  LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement 934872 gene
                                                                                  NAME/KEY: exon
LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement 934872 gene
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
MAME/KEX:
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
                                                                                                                                                                      NAME/KEY: exon
LOCATION: 240528..241685
OTHER INFORMATION: exon M1 complement g34872 gene
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; Patent No. 6555316
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Matches 142; Conservative
exon 240528..240824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 292653..292841
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APPLICANT: Cohen, I
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NAME/KEY: allele
LOCATION: 202679
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LOCATION: 203378
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LOCATION: 207313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: 209123
                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: 189957
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LOCATION: 208285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 209631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 99-31960-363 ; polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 99-24639-163 : polymorphic base A or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 21672
OTHER INFORMATION: 99-27935-193 : polymorphic base G or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 107281 . OTHER . OTHER . THORMATION: 99-24656-260 : polymorphic base A or NAME/KEY: allele LOCATION: 166640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 8-128-33 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 246273..247802
OTHER INFORMATION: exon Z
NAME/KEY: misc_feature
LCCATION: 247803..249803
OTHER INFORMATION: 3/regulatory region
NAME/KEY: allele
                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 199122..201122
OTHER INFORMATION: 5'regulatory region
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HER INFORMATION: exon V2
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INFORMATION: exon V1
                                                                                                                                                                                                                                                                                                    INFORMATION: exon S2
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THER INFORMATION: exon V4
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134
                                                                                                                                                                                                                   LOCATION: 201123..201234
OTHER INFORMATION: exon S
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: exon V
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THER INFORMATION: exon Y
AME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                               THER INFORMATION: exon T
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                                                                                              ORGANISM: Homo sapiens
NUMBER OF SEQ ID NOS:
                  Patent.pm
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LOCATION: 95396
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LOCATION: 65485
                SOFTWARE: Paten
SEQ ID NO 1
LENGTH: 319608
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                                                                             TYPE: DNA
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NAME/KEY: allele
LOCATION: 204934
OTHER INFORMATION: 99-24644-194 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 205206
OTHER INFORMATION: 8-295-248 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 205329
OTHER INFORMATION: 8-295-125 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2050664
OTHER INFORMATION: 8-293-130 : polymorphic base A or G OTHER INFORMATION: 99-5919-215 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 197163
OTHER INFORMATION: 99-24658-410 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 200778
OTHER INFORMATION: 8-303-235 : polymorphic base A or G Ö LOCATION: 160876 OTHER INFORMATION: 99-24634-108 : polymorphic base A or T OTHER INFORMATION: 99-16100-147 : polymorphic base A or G : polymorphic base A or G : polymorphic base A or G NAME/KEY: allele
LOCATION: 204138
OTHER INFORMATION: 8-296-213 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 204605
OTHER INFORMATION: 8-252-190 : polymorphic base C or T OTHER INFORMATION: 8-283-176 : polymorphic base A or G NAME/KEY: allele : polymorphic base A or G : polymorphic base C or T : polymorphic base A or G : polymorphic base G or C : polymorphic base A or T : polymorphic base A or G OTHER INFORMATION: 8-287-86 : polymorphic base A or NAME/KEY: allele LOCATION: 173358 OTHER INFORMATION: 99-5862-167 OTHER INFORMATION: 99-7652-162 NAME/KEY: allele LOCATION: 206545 OTHER INFORMATION: 8-292-198 OTHER INFORMATION: 8-289-322 NAME/KEY: allele LOCATION: 208960 OTHER INFORMATION: 8-287-249 NAME/KEY: allele LOCATION: 202651 OTHER INFORMATION: 8-300-221 DTHER INFORMATION: 8-300-193 OTHER INFORMATION: 8-299-128 OTHER INFORMATION: 8-285-319 OTHER INFORMATION: 8-283-278 OTHER INFORMATION: 8-251-322

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PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
LENGTH: 162450
                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 9
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LOCATION: 93714
OTHER INFORMATION:
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INFORMATION:
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INFORMATION:
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LOCATION: 103806
OTHER INFORMATION:
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INFORMATION:
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INFORMATION:
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LOCATION: 106940
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 72794
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LOCATION: 88073
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LOCATION: 108106
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                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                            : variable motif AAAGG or GAAGGAAGGAAGGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 GTACAATCCAACCCTTTGAGAGGTTAATGTGTGTGCGGATTTTTCTAGATAAACAAGGYGC 298
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Pred. No. 0.00017;
1; Mismatches 92; Indels 8;
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APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH
FILE REPERENCE: GENEST.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
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Patent No. 6399373
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 211366
OTHER INFORMATION: 8-281-248:
NAME/KEY: allele
LOCATION: 212520
OTHER INFORMATION: 8-279-197:
LOCATION: 210486
OTHER INFORMATION: 8-283-153
NAME/KEY: allele
                                                                                   NAME/KEY: allele
LOCATION: 210879
OTHER INFORMATION: 8-282-345
LOCATION: 210964
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                                                                                                                                                                       OTHER INFORMATION: 8-282-260
NAME/KEY: allele
LOCATION: 210979
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Best Local Similarity 58.4%;
Matches 142; Conservative
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                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: 211050
OTHER INFORMATION: 8-282-174
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LOCATION: 211132
OTHER INFORMATION: 8-282-92
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                                                     LOCATION: 210583
OTHER INFORMATION:
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LOCATION: 211247
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LOCATION: 211315
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LOCATION: 212821
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                                                    99-1437-325
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5-124-273
                         OTHER INFORMATION: 5-127-261
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us-09-647-841b-1.rni

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Query Match 4.3%; Score 69.2; DB 4; Length 162450; Best Local Similarity 62.9%; Pred. No. 0.00017; Matches 107; Conservative 0; Mismatches 63; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROCEDURES AND REGULATORY DNA SEQUENCES; FOR GENETICALLY ENGINEERING DISEASE RESISTANCE AND OTHER; INDUCIBLE TRAITS IN PLANTS
; UNUMBER OF SEQUENCISS: 9
; CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37.
                                                                                                                                                                     NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COCATION: 108184...108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127...108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEX: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
                                                                                                                 LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: allele
COCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
                                                         OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
                                                                                                                                                                                                                                                                                     INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
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;Patent No. 5312912
; APPLICANT: HADWIGER, LEE A.;CHIANG, CHIN C.;HOROVITZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: polymorphic fragment 5-133-375 | FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375
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LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
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LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
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CON: 72771..72817
INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
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LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
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OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
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LOCATION: 93690..93736
OTHER INFORMATION: Polymorphic fragment 5-128-60 SEQ ID32
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261
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OTHER INFORMATION: 5-140-348 :
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                                                                                                                                                 INFORMATION: 5-143-84
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FEATURE:
                                                         ION: 134374
INFORMATION:
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INFORMATION:
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Patent No. 6020318

GENERAL INFORMATION:
APPLICANT: Szyf, Moshe
APPLICANT: Bagey, Pascal
APPLICANT: Ranchandani, Shyam
TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
                                                                                                           DB 6; Length 1890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 4084;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                           Score 69; DB 6;
Pred. No. 0.0001;
0; Mismatches 7
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ATTORNEY/AGENT INFORMATION:
NAME: RECOWN, WARDNER: 33,923
REFERENCE/DOCKET NUMBER: 166.101.187
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/07/393,301 FILING DATE: 13-JUN-1989;SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
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60 State Street
                                                                                                          4.3%;
                                                                                                        Query Match
Best Local Similarity 60.34
Matches 108; Conservative
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Best Local Similarity 62.45
Matches 108; Conservative
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STRANDEDNESS: both
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CITY: Boston
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US-08-866-340-1
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Search completed: August 14, 2003, 21:49:30 Job time : 119 secs

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206, App
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528, App
478, App
138, App
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138, App
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| Cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/DCT_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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version 5.1.6
- 2003 Compugen Ltd.
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US-10-311-455-5

US-10-10-206-110

US-10-240-453-206

US-10-311-455-288

US-10-074-045-60

US-10-074-045-208

US-10-172-086-10

US-10-172-086-10

US-10-172-086-10

US-10-172-086-10

US-10-172-086-10

US-10-1311-455-528

US-10-240-485-138

US-10-240-485-138

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US-10-11-455-527
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    nucleic search, using sw model
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Copyright (c) 1993
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Maximum DB seq length: 2000000000
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Perfect score:
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ALIGNMENTS

US-10-311-455-288

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10311 A1 LStia	3 of 3 met 35/10 2-16 1/EPC	1004	se Ly tr	9	rttig rtage	PATAT ATAT
See Application US/103114 To US20030143606A1 WATION: PIEK, Alexander PIEPENBROCK, Christian	nosis osine 4 ER: (02-1; 07-0;	06-3(: DE 09-0;	quenc ical]	65.8 8.58 8.58	TTAAGCTYGATAATAATTTT ATAATTTAGATTTTTATTAG	TATA:
tion 3014 xand	Kurt Diag Cytic 101 NUMB NUMB MBER 001-	000- MBER 000- : 24	l Se chem	4 vati	GATA GATT	TATA TATA
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No.10'-31-433-288 Sequence 288, Application US/10311455 Publication No. US20030143606A1 GENERAL INFORMATION: APPLICANT: OLEK, Alexander APPLICANT: PIEPENBNOCK, Christian	APPLICANT: BERLIN, Kurt TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by TITLE OF INVENTION: CYtOSINE methylation FILE REFERENCE: 5013:1014 CURRENT APPLICATION NUMBER: US/10/311,455 CURRENT FILING DATE: 2002-12-16 PRIOR APPLICATION NUMBER: PCT/EP01/07537 PRIOR APPLICATION NUMBER: DE 10032529.7	PRIOR FILING DATE: ::000-06-30 PRIOR APPLICATION NUMBER: DE 10043826.1 PRIOR FILING DATE: ::000-09-01 NUMBER OF SEQ ID NOS: 2424 SEQ ID NO 288 LENGTH: 6641 TYPE: DAA	ORGANISM: Artificial Sequence FEATURE: CTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)	Query Match 5.8%; Best Local Similarity 46.5%; Matches 451; Conservative	. ~	5
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Publication No. US20030113750A1

GENERAL INFORMATION:

APPLICANT: Epigenomics AG

TITLE OF INVENTION: Method and nucleic acids for the differentiation

TITLE OF INVENTION: Of prostate tumors

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/172,086

CURRENT FILING DATE: 2002-06-13
                                                                                                                                                                                                                             ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-5
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Pred. No. 0.00038;
0; Mismatches 96;
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Best Local Similarity 61.9%; Pred. No. 0.00039;
Matches 146; Conservative 0; Mismatches 90;
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 116
SEQ ID NO 10
                                                                                                                                                                                               ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 61.0%;
Matches 150; Conservative
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US-10-172-086-10
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Publication No. US20030143606A1
GENERAL INFORMATION:
SEQUENCE APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
FILE REFERENCE: 5013.1014
                                  2873
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                   431 AAAAAAAAAAGTCATAAATATAGTTTATACATATAACTTTAATAAAAAATAAAAATTTCA 490
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                                                                               191 GGTAAAAAATAAATATATATTTGTTACCATTTAAAAGTCATAAATATAGTACAATCCAAC
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            APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune Syst
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
FRICH REPRICATION NUMBER: DFT/FP01/07537
PRIOR FILING DATE: 3001-07-02
PRIOR FILING DATE: 3000-06-30
SEQ ID NOS: 2424
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Local Similarity 49.9%; Pred. No. 0.00048;
hes 285; Conservative 0; Mismatches 281;
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      PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Best Local S
Matches 285
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: DLEK, Alexander
APPLICANT: BERLIN; Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: Dy Means of Assessing the Methylation Status of Genes Associated
TITLE OF INVENTION: With DNA TRANScription
TITLE OF INVENTION: With DNA TRANScription
TITLE OF INVENTION: With DNA TRANScription
FILE REFERENCE: 5013.1009
CURRENT FILING DATE: 2002-10-02
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-08-30
                    237
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                                                                            182 TACGTTGATGGTAAAAAAAATAATATATTTGTTACCATTTAAAAGTCATAAATAT
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Pred. No. 0.00051;
0; Mismatches 69;
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                                                                                                                                                                                                             Sequence 206, Application US/10240453 Publication No. US20030148326A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%;
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Best Local Similarity 65.8<sup>3</sup>
Matches 133; Conservative
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; LOCATION: (9105)
US-10-240-453-206
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US-10-311-455-288/c
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us-09-647-841b-1.rnpb

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Sequence 20. Application US/10240453
; Sequence 20. Application No. US2003014832641
; Sequence 20. Application No. US2003014832641
; GENERAL INFORMATION:
    APPLICANT: OLEK, ALexander:
    APPLICANT: DLEK, ALExander:
    APPLICANT: PIEPENBROCK, Christian
    APPLICANT: PIEPENBROCK, Christian
    APPLICANT: PIEPENBROCK, Christian
    APPLICANT: BERLIN, Kurt
    TITLE OF INVEWTION: Diagnosis of Diseases Associated with DNA
    TITLE OF INVEWTION: With DNA TRanscription
    TITLE OF INVEWTION: With DNA TRAnscription
    TITLE OF INVEWTION: With DNA TRANSCRIPTION
    TITLE NEFERENCE: 2013.1009
    CURRENT FILING DATE: 2002-10-02
    PRIOR PILICATION NUMBER: DE 10019058.8
    PRIOR FILING DATE: 2000-04-06
    PRIOR FILING DATE: 2000-04-06
    PRIOR FILING DATE: 2000-04-07
    PRIOR FILING DATE: 2000-06-30
    PRIOR FILING DATE: 2000-09-01
    NUMBER OF SEQ ID NOS: 350
    LEWICH: 11745
    LEWICH: INTAS
                                                                AAAAAATAAATATATTTGTTACCATTTAAAAGTCATAAATATAGTACAATCC
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US-10-172-086-10/c
; Sequence 10, Application US/10172086
; Publication No. US20030113750A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: unsure
; LOCATION: (9105)
US-10-240-453-206
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Sequence 528, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: DEMENSOCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.101

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR PPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-09-01

SED ID NO 528

LENGTH: 9136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 ATATATATATATATATATATATATATAATATTTTATTTACCAATTTAAAATTATATAT 134
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                                                                                                                                                                                                                                                                            Score 91; DB 14; Length 3991;
Pred. No. 0.00048;
0; Mismatches 80; Indels
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT2010.

CURRENT APPLICATION NUMBER: US/10/074,045

CURRENT FILING DATE: 2002-02-14

PILOT APPLICATION TEMOVED - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 60
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Best Local Similarity 64.4%;
Matches 154; Conservative 0
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US-10-074-045-60
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Associated with the Immune System by
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Best Local Similarity 68.1%; Pred. No. 0.001;
Matches 124; Conservative 0; Mismatches 58;
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Cytosine methylation
FILE REPERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR FAPLICATION NUMBER: US/10/311,455
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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LENGTH: 8136
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APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Parsons, Jeremy D.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Soybean Cyst Nematode Resistance File Repersence: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
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               APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method and nucleic acids for the differentiation
TITLE OF INVENTION: of prostate tumors
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/172,086
CURRENT FILING DATE: 2002-06-13
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 513509;
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Pred. No. 0.00092;
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Pred. No. 0.0026;
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; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 318013_region_A3
US-09-754-853A-4
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                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 68.7%;
Matches 123; Conservative
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Best Local Similarity 47.5%;
Matches 296; Conservative
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GENERAL INFORMATION:
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Db 2363 TGTTAAA-ATTATTAATAATAATAATATTATATTATATT	Oy 602 CATTGGTTAAAAAA 616 Db 2602 GAATTATAAAAGGAA 2616 RESULT 13 US-10-240-485-138 US-10-240-485-138 Sequence 138, Application US/10240485 Publication No. US20030148327A1 SERRAL INFORMATION: APPLICANT: DIEPENBROCK, Christian APPLICANT: DAEN AUGUST 2001-02 CURRENT APPLICATION: Metastasis FILE REFERENCE: 5013 1010-02 FRIOR APPLICATION NUMBER: US/10/240,485 PRIOR FILING DATE: 2001-04-06 PRIOR FILING DATE: 2000-04-07 PRIOR PELING DATE: 2000-04-07 PRIOR PELING DATE: 2000-04-07 PRIOR PELING DATE: 2000-04-07 PRIOR PELING DATE: 2000-06-30 PRIOR PELING DATE: 2000-06-30 PRIOR PELING DATE: 2000-06-30 PRIOR PELING DATE: 2000-06-30 PRIOR PELING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 202 SEQ ID NO 138 LENGTH: 14551 TYPE: DNA OFHER INFORMATION: Chemically treated denomic DNA (Homo saplens) OTHER INFORMATION: Chemically treated	7.4; DB 12; Lengt 5. 0.0021; atches 71; Indel	15 AAGCTTGATAATTTTGCGATCTATATATAAGCCCACTACCAATTTAAAATTATATATA	Qỳ 75 ATATATATATATATATATATATATAATAATTTTATTACCAATTTAAAATTATATA 134	Db 2930 ATATAGATATATATATATATATATATATATATATATATA	
Db 7101 TTATTTATATATATATAGAGATTTATAGAGATTTATATATATATATATATAT 7160 Qy 61 TTAAAATTATATATATATATATATATATATATATATAT	SULT 12 Sequenc Sequenc Publica Septic APPLIC APPLIC TITLE TITLE TITLE TITLE PRIOR P	AGAT PATA PATT	122 TAAAATTATATATATATATATATATATATATATATAT	OY 182 TACGTIGATGGTAAAAAAAAAAATAAATTTGTTACCATTTAAAAGTCATAAATATGTA 241	Db 2243 ATTALATATATAGATTTATTAAGGATATGTTGGTGGAAATTTTATTTGT 2302 Qy 302 TCACGATTCTTGGTGCAGGCTTGGAGAACCCTATCCTGGGCTTGGAGATTTACTTCT 361 Db 2303 TTTAGATTGAGAAGGAATTAGGAATTAATGTGAAGCAAATTTAAAAAAAA	

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Search completed: August 14, 2003, 23:27:34 Job time : 439 secs
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                                Sequence 527, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: DIEPENBROCK, Christian

APPLICANT: DIEPENBROCK, Christian

APPLICANT: DEELLOW Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern

TITLE OF INVENTION: DATE: 2002-12-16

PRIOR FILING DATE: 2002-12-16

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NOS: 2424
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TITLE OF INVENTION: Metastasis
FILE REPERENCE: 5013.1007
CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT FILING DATE: 2002-10-02
PRIOR PRICEDATION NUMBER: US/TEP01/03970
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 202
SEQ ID NO 138
LENGTH: 14551
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Publication No. US20030148327A1
GENERAL INFORMATION:
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
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                    US-10-311-455-527/c
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-485-138
                                               Length 14551;
                                                                                  Indels
                                               Query Match 5.4%; Score 87.2; DB 12; Best Local Similarity 66.5%; Pred. No. 0.0023; Matches 125; Conservative 0; Mismatches 63;
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AL565455 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF005Y0:8 3-PRIME, mRNA sequence.
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Tetraodon Danio rer

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BX204248 CC134240 BX143241 CNS04707 BX165235 CNS04707

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Li (bases I to 1201)
Li W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
On Feb 16, 2001 this sequence version replaced gi:12916848.
Contact: Genoscope Genoscope Tentre National de Sequencage
BP 191 91006 EVRY cedex - France Homo sapiens (human)

Email: sequefgenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODF005BH09NPl&cluster=9232.f. Contact:
Feng Liang Email : fliang@lifetech.com URL :

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/db_txref="taxon:9600"
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/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)
Eul, W.B., Gruber, C., Jessee, J. and Polayes, D. Ful, Hength CDNA libraries and normalization
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Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF005BH09NPlscluster=9232.f. Contact:
http://willength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF005BH09NPl.
Location/Qualifiers
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                                                    GITAAGCATAAAAACATCAAAGTCTAGCAAAATGTTGTTTTTGCGATGACAT
                                                                                Query Match
7.1%; Score 115; DB 9; Length 1201;
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Matches 277; Conservative 122; Mismatches 337; Indels
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http://fulllength.invitrogen.com/
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Library was not normalized." BASE COUNT 515 a 30 c 71 g 310 t 274 others ORIGIN	Query Match 6.8%; Score 109.6; DB 13; Length 1200; Best Local Similarity 32.2%; Pred. No. 0.04; Matches 308; Conservative 183; Mismatches 462; Indels 3; Gaps 2;	QY 1 TTTAPAAATATTTAAGCTTGATAATAATTTGCGATCTATATAAGCCCACTACCAAT 60	QY 61 TTAAAATTATATATATATATATATATATATATATATAT	QY 121 TTAAATTATATATATATATATATATATATATATATATA	Qy 181 TTACGTTGATAAAAAAAAATAAATTGTTACCATTTAAAAGTCATAAATATAGT 240	QY 241 ACAATCCAACCCTTGAGAGGTTAATGTGTGGGGATTTTCTAGATAAACAAGGYGCCA 300 1	QY 301 TTCACGATYCTTCTTGGTGCAGCTTGGAGACCCTATCCTGGGCTTGGAAGATTTACTTC 360	QY 361 TIGITGATGCTTCTAGAGTACAGCTCCTTAAGGCTGTAGTTTTTTTT	QY 421 TCCTACCAAAAAAAAAGTCATAAATATAGTTTATACATATAACTTTAATAAAAATAA 480 1 : : : : : : :	QY 481.AAAAATTCATCCCTAAAAACATAGTAGAAATTTCATAAAAAAATTTGTTATAATTT 540 : ::::	OY 541 ACATGCCGTAAAAAATGGATAAATTGGGTATGGAGTACTAGTAATAATAAGGT 600 :::	OY 601 TCATTGGTTAAAAAACTAAAAAATAATTTCGGTCCTGATTTATATGAAATGACATTTTT 660 11 11 11 11 11 11 11 11 11 11 11 11 11	QY 721 TGAATATAGATTTTGGGCGATCAAACACAAGAATCATTACGATAACATGCTTATACATA 780	QY 781 CCCCGTCAATCTTTTTTACCCAATAAACATGAAATGTTGCTTCTTTGGTTAAGC 840 ::: ::: ::: ::: Db 333 AAAMHYYYTTAWAWWWAAAWHCCCCCAATHHTWATCHWATYTTTWWWATTTTT 274	QY 841 ATAAAAACTTCAAAGTCTAGCAAAATGTTGTTTTTGCGATGACACATTCATATAGTTTA 900	OY 901 AAGGATGCATGATTACAAAAACAAAATACTAATAATTCTAGCACAAAGTTT 956 1 1 1 1 1 1 1 1 1	
QY 282 CTAGATAAAGAGGYGCCATTCACGATTCTTGTGGTGCAGCTTGGAGAACCTATCTG 341 :	QY 34.2 GGCTTGGAAGATTTACTTCTTGTTGATGCTCTGAGGGTCCTTAAGGCTGTAGTC 401	QY 402 TAGTTTTTTTTTTCATCCTTCCTACCAAAAAAAAAAAAA	QY 462 ATAACTTTAATAAAAAATATCACCCCTAAAAACATAGTÁGAAATTTCATAAAA 521 	OY 522 AAAATATTGTTTATAATTTACATGCCGTTACGGTAAAAATGGATAAATTGGGTATGGG 581 	OY 582 TACTAGTAATTAATAAGGTTCATTGGTTAAAAAACTAAAAAATATTCTCTCCTGATT 641	QY 642 TATATGAAATGACATTTTTTGGAACATGAAGGGTATTGATTTTACCACCTTTTACACC 701 	OY 702 TITCAAAGCCATTCAAGGATGAATATAGATTTTTGGGCGATCAAACAAGAATCATTAC 761 	OY 762 GATAACATGCTTATACATA 780 Db 1136 ATAWATAWATAWA 1154	BX437758 1200 bp mRNA linear EST 15-MA	7B01	S EST. Homo sapiens (human) ISM Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE I (bases 1 to 1200) AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.	BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :	http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOCAPO08CA01QP1. Location/Qualifiers source 11200	/organism="Homo Sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSOCAP008XB01"	/Clone_lib="HATMUS" /Clone_lib="Homo sapiens THYMUS" /note="Vector: pCMVSPORT_6; lst strand cDNA was primed with a NotI-rollgo(dT) primer. Five prime end enriched, Anhlosetessa Anna sincet and allowed site.	<pre>double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.</pre>

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/ Organism="Homo saplens"
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full length cDNA libraries and normalization
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         TIWATWAATITIATAAWIAAAATTASAAAAWITITITITITITITATITIWAATTIWAAT
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : filang@lifetech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP00BBE0120F1.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Linvitrogen. Contact : Feng Liang Email : filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO08BE02QP1.
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Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/organism="Homo saplens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone="vector: pCMVSPORT_6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized."
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 http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0CAP004AD10NP1. Location/Qualifiers
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Matches 216; Conservative 99; Mismatches ;
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                                                                                                                                                                                       Direct Submission Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished This sequence was generated from the T7 end of BAC 46L20. 46L20 is part of the Danlokey BAC Library created by R. Plasterk and N.V.
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BP 191 91006 EVRY cedex - France
Email: seqreféqenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fillang@lifetech.com URL :
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Cypriniformes; Cyprinidae; Danio.

I (bases i to 400)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Direct Submission
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Li,W. B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Pred. No. 0.29;
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/tissue_type="Testis"
/note="vector pindigoBAC-536"
33 c 35 g 164 t
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                                                                                                                                                                                                                                                                                                                                                                 /organism="Danio rerio"
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/db_xref="taxon:7955"
                                AL974628.1 GI:25185789
                                                                      Danio rerio (zebrafish)
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71.28;
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Contact: Genoscope
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

(Syrinifornes; Cyprinidae; Danio.

1 (Dases : to 490)

Humphray, S. J., Huckle, E. and Durham, J. L.

Direct Submitsed (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campue, Hinxton, Cambidgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                        BX237235 490 bp DNA linear GSS 29-JAN-2003 Danio rerio genomic clone DKEY-283H15, genomic survey sequence. BX237235
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                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 TATTACGTTGATGCTAAAAAAAATATATATTTGTTACCATTTAAAAGTCATAAATATA
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/note="vector pindigoBAC-536"
32 c 35 g 219 t
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72.8%; Pred. No. 0.36;
tive 0; Mismatches
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/db_xref="taxon:7955"
/clone="DKEY-283H15"
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//organism="Oryza sativa (japonica cultivar-group)"
//organism="Oryza sativa (japonica cultivar-group)"
//strain="Japonica"
//clultivar="Nipponica"
//clultivar="Nipponica"
//clone="nebolo2Fro6r"
//tissue_type="Leaf"
//lab_host="Leaf"
//la
                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzeae; Oryza.
I (bases 1 to 797)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
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                                                                                                                                                                                                                                                                                                   Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jozdan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
Seg primer: GGAAACAGCTATGACCATG
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High quality sequence stop: 329.
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                     AQ868440.1 GI:6218891
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I (bases 1 to 698)

Humphray, S. J., Huckle, E. and Durham, J. L.

Direct Submission

Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 223D6. 223D6 1s part of the Danlokey BAC Library created by R. Plasterk and N.V.

Keygene. Further details:
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danlo.
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Danio rerio genomic clone DKEY-223D6, genomic survey sequence.
BX200889
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Pred. No. 0.44;
0; Mismatches 60; Indels
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   /tissue_type="Testis"
/note="vector pindigoBAC-536"
117 c 78 g 252 t
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/note="vector pindigoBAC-536"
97 c 66 g 245 t
                                                                                            Score 100.6; DE
Pred. No. 0.38;
0; Mismatches
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/db_xref="taxon:7955"
/clone="DKEY-223D6"
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Best Local Similarity 64.3%;
Matches 151; Conservative
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Best Local Similarity 69.4%;
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Humphray, S.J., Huckle, E. and Durham, J.L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 258122. 258122
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
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BX153480
BX153480.1 GI:27985037
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1 (bases 1 to 707)

Humphray,S.J., Huckle,E. and Durham,J.L.
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Location/Qualifiers
                                                                                                                                                http://www.sanger:ac.uk/Projects/D_rerio/
Location/Qualifiers
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Pred. No. 0.42;
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Best Local Similarity 65.5%;
Matches 163; Conservative (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

E 1 (bases 1 to 605)

S Humphray, S. J., Huckle, E. and Durham, J.L.

Direct Submission

L Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished from the T7 end of BAC 145x15. 145x15 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene: Further details:

http://www.sanger.ac.uk/Projects/D_rerio/.
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a 84 c 85 g 211 t
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
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                                         Danio rerio (zebrafish)
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/db_txref="taxon:9606"
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/note="Vector: pCMYSPORT_6; lst strand cloned into
the Not I and EcoNY sites of the pCMYSPORT 6 vector.
Library was not normalized."
Library was not normalized."

105 g 370 t 196 others
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Genoscope
Genoscope
BP 191 91006 EVRI codex - France
BB 191 91006 EVRI codex - France
BBall: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Bmall: filangelifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden. Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA010ZB0IFPI.
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Danio rerio genomic clone DKEY-145K15, genomic survey sequence.
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1 (bases 1 to 1201)
Liw.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Pred. No. 0.34;
3; Mismatches 81; Indels 1
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BX446511.1 GI:31019733
                                                                               148 AAAATTCAGGGGCAAT 133
                                         216 ACCATTTAAAAGTCAT 231
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Best Local Similarity 64.3%;
Matches 153; Conservative
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